PROCEEDINGS OF TDWG

Biodiversity Information Science and Standards 1: e20219
doi: 10.3897/tdwgproceedings.1.20219

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Conference Abstract

The Taxonomic and Biodiversity Software Stack in R

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Received: 11 Aug 2017 | Published: 12 Aug 2017

Citation: Chamberlain S (2017) The Taxonomic and Biodiversity Software Stack in R. Proceedings of TDWG 1: e20219. https://doi.org/10.3897/tdwgproceedings.1.20219

Abstract

High quality R software for taxonomy and biodiversity occurrence data are important, both because there are a large number of biologists who use R, and because R allows reproducible and open science. I will do an overview of the software that our non-profit organization rOpenSci (https://ropensci.org) produces for both taxonomy and biodiversity work, their use cases, and future improvements. In addition, I will provide details about our latest work on software that defines taxonomic classes for consistent and powerful manipulations of taxonomic data (for example, select certain taxonomic names, and associated data are selected for those taxa). Finally, I will discuss new R software (pegax (https://github.com/ropenscilabs/pegax)) for high performance taxonomic name parsing, which will allow fast and operating system independent parsing of taxonomic names.

Keywords

taxonomy, software, R, rstats

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